

GenCore version 5.1.4-p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 16:50:06 ; Search time 0.001 Seconds

(without alignments)  
2318.058 Million cell updates/sec

Title: us-09-854-280-4 ←

Perfect score: 1047  
Sequence: 1 gccaggtgtcagcgcgtc.....tgatgaacacatcccaaaa 1047

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 1107 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: us-09-480-297a-22: \* ←

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1028.9	98.3	1107	1	us-09-480-297a-22
2	34.4	3.3	1107	1	us-09-480-297a-22

## ALIGNMENTS

RESULT 1  
us-09-480-297a-22

Query Match 98.3%; Score 1028.9; DB 1; Length 1107;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1040; Conservative 0; Mismatches 1; Indels 50; Gaps 1;

QY	1	GCCAGGTGTCAGAGCGGCTCAAGCCAGCCCTGCGCGCCACCATGAGCGTCT	60
DB	66	GCCAGGTGTCAGAGCGGCTCAAGCCAGCCCTGCGCGCCACCATGAGCGTCT	125
QY	61	CCCCGGGCTCTGTTTGTGACGTGTCAGACATGCTGGCCACCATGAGCGTCT	120
DB	126	CCCCGGGCTCTGTTTGTGACGTGTCAGACATGCTGGCCACCATGAGCGTCT	185
QY	121	CAGGGGGACACCCACAGTACAGGTACCCACACTGCTACTGAGTGAAGTGCCT	180
DB	186	CAGGGGGACACCCACAGTACAGGTACCCACACTGCTACTGAGTGAAGTGCCT	245
QY	181	CGGCGAGGCCCCCACACTGCTGCTGTCAGAGTGCCTGAGGAGGAGGCTTTCCT	240
DB	246	CGGCGAGGCCCCCACACTGCTGCTGTCAGAGTGCCTGAGGAGGAGGCTTTCCT	305
QY	241	AGCCCTGTGTGTCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	300
DB	306	AGCCCTGTGTGTCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	365

RESULT 2  
us-09-480-297a-22/c

Query Match 3.3%; Score 34.4; DB 1; Length 1107;  
Best Local Similarity 52.9%; Pred. No. 0;  
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY	190	CCCCACACCTCTGCTGAGTGCAGAGTGGGGAGAGGCTTGTAGCCCTGT	249
DB	394	CGGCGGACACACCGGCACTGGGTCTGACTGAGGCTCTGCTGCTGCTGCTG	335
QY	250	GTCAGGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	309
DB	334	TTGCTGCTTCCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	275
QY	310	GTCGCGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	329
DB	274	GAGCCAGAGGTGTGGGGG	255

GenCore version 5.1.4.p5.4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 20, 2003, 06:52:11 ; Search time 1 seconds

(without alignments)  
0.436 Million cell updates/sec

Title: us-09-854-280-3

Sequence: 1 MILPLGLELFWLHTCLAH.....FHTEFHPVGGCTCVLPRSV 197

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 1107 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=soft -O=us-09-854-280-3 -DB=us-09-480-297a-22  
-SUFFIX=pro -OUT=align\_3\_22 -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -UNITS=bits  
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200  
-THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO\_XLPXY  
-NEG\_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database: us-09-480-297a-22:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1073	100.0	1107	1	us-09-480-297a-22

#### ALIGNMENTS

RESULT 1  
us-09-480-297a-22

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0	1073.00	100.008	100.008	1	1107	197	0	0	0	0

us-09-854-280-3 (1-197) x us-09-480-297a-22 (1-1107)

QY 1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuValAlaHisHis 20  
DB 115 ATGACGCTCCCTCCGCGGCTCTGTTCTGACCTGCGGCTGACACATGCTGCGCCACCAT 174

QY 21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40  
DB 175 GACCCCTCCCTCAGGGGGGACCCCCACAGTCACGGTACCCACACTCTACTCGGGCTAG 234  
QY 41 GluLeuProLeuGlyAlaAlaProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60  
DB 235 GAACGGCCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 294  
QY 61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisAlaArgGlyHisGlu 80  
DB 295 GCTTGGCTGTACCCCTGGGTGTCCAGCTGAGGACAGCCAGGAGGAGGAGGAGGAGGAGG 354  
QY 81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100  
DB 355 AGGCTTCACCTACGACCCAGCCAGTGGCGGCTGCTGGCGGCGGCGGCGGCGGCGGCGG 414  
QY 101 ThrHisGlnArgSerHisSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120  
DB 415 ACCCAGCAGCGGCTCCATCTCACCCTGGAGATACCGTGTGACACGAGATGAGGAGCGCTAT 474  
QY 121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140  
DB 475 CCACAGAGAGCTGGCTTCGCGGAGTGGCTGTGACAGGCTGTATCGATGACAGGAGCGGC 534  
QY 141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160  
DB 535 CGCAGACAGCTGGCTTCACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594  
QY 161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaHisThr 180  
DB 595 CGGCCCTGCTCCCGCGGAGGCTGGGCTGCCACACTGGGCGCTTGGCTTCCACACC 654  
QY 181 GluPheLeuHisValProValGlyCysThrCysValLeuProAlaGlySerVal 197  
DB 655 GAGTTCATCCACGTCGCCGCTGCGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705

Search completed: May 20, 2003, 06:52:12  
Job time: 1 secs

Db 1 MTLLPGLFLFTWHTCLAHNDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLARGAQWQ 60  
QY 61 ALPVAVSSLEAASHRGHERPSATTQCPLRPEEVLADTHQRSISPWRVETDEDRY 120  
Db 61 ALPVAVSSLEAASHRGHERPSATTQCPLRPEEVLADTHQRSISPWRVETDEDRY 120  
QY 121 POKLAFBECICRGCIDARTGREPALNSVRLQSLVLRRRPCCRDSGLPTPGAFAFHT 180  
Db 121 POKLAFBECICRGCIDARTGREPALNSVRLQSLVLRRRPCCRDSGLPTPGAFAFHT 180  
QY 181 EFTHVPGCTCVLP RSV 197  
Db 181 EFTHVPGCTCVLP RSV 197

RESULT 6  
US-09-480-297A-23  
Sequence 23, Application US/09480297A

GENERAL INFORMATION:  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Kastelein, Robert A.  
TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS  
FILE REFERENCE: DX0917K  
CURRENT APPLICATION NUMBER: US/09/480, 297A  
CURRENT FILING DATE: 2000-01-10  
PRIOR APPLICATION NUMBER: 60/115,506  
PRIOR FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 197  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-480-297A-23

Query Match 100.0%; Score 1073; DB 18; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2.7e-98;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTLLPGLFLFTWHTCLAHNDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLARGAQWQ 60